

FIGURE 1

Alignment of Biotin Synthase Proteins from Barley (SID18), Corn (SID 20-24), Prickly Poppy (SID 28), Soybean (SID 28 and 30), and Wheat (SID 32)

SID18	TTTPS-----AVSP--SAAAAPFRPALLAE--PAMMLLARSSLRSVRSPFASAVSAAPFSSVSSAAAAAERAVERAVRDGPRNDWTRP	EIQAIYDSPLLDLLFHGAQVHRNVHKFREVQQCTLLSIKTGGCSEDCSYCPQSSRYSTGLKAEKLMKKDAVLEAKKAKEAGSTRFCMGA			
SID20	MA-----	EIQAVYDSPLLDLLFHGAQVHRNVHKFREVQQCTLLSIKTGGCSEDCSYCPQSSRYNTGLKAEKLMNKYAVLEAKKAKEAGSTRFCMGA			
SID22	MA-----	EIQAVYDSPLLDLLFHGAQVHRNVHKFREVQQCTLLSIKTGGCSEDCSYCPQSSRYNTGLKAEKLMNKDAVLEAKKAKEAGSTRFCMGA			
SID24	MA-----	EIQAVYDSPLLDLLFHGAQVHRNVHKFREVQQCTLLSIKTGGCSEDCSYCPQSSRYNTGLKAEKLMNKDAVLEAKKAKEAGSTRFCMGA			
SID26	--	EIKSVYDSPVLDLLFHAAQVHRRAHNFRREVQQCTLLSVKTTGGCSEDCSYCPQSSRYDTGVKAQKLMNKDAVLOAAEKAKEAGSTRFCMGA			
SID28	TKPNPKHKKYRCCULLSLSCLYSQISHFSVSVLSPNFEFESKNMFLARPIFRA--PSLWALHSSAYSSASSAAIQAERAIKEGPRNDWSRD	QVKSIYDSPVLDLLFHGAQVHRRAHNFRREVQQCTLLSIKTGGCSEDCSYCPQSSRYSKYDTGVKGQLMNKEAVLQAAKKAKEAGSTRFCMGA			
SID32	T--	EIKSVYDSPVLDLLFHGAQVHRRAHNFRREVQQCTLLSIKTGGCSEDCSYCPQSSRYNTGLKAEKLMNKDAVLEAKKAKEAGSTRFCMGA			
1705463	--	1705463	--	--MMLVRSVFRSQ--	--SSVRLQVOKSRNYGTVSSVPQATESTSSTSPSKDVYQEALNATE-PRSNWTRE
SID30	MAT-----	SID30	M-	LRTSLSRSLLLRSNTPKLAPIS--	-LRPSV-SG-----GLQSACSYSSLSAASAAERTIREGPRNDWSRD
2995363	M-----	2995363	M-----	FT-----RTIIRQIRRSSALSIV--	-RNNWTRE
6321725	M-----	6321725	M-----	MSTIYRHLSTA--RPALTKYATNAAA--	-VKSSTTASSEASTLGALQYALSLI-----DEPSHSWTKS

FIGURE 1 (page 2 of 2)

SID18	AWRETTIGRKNSNENQILEYVKKD1RGGMGMEVCCCTLGMILEKQQAEEELKKAGLTAYNHNLDTSRSEYYPNIIISTSYSYDDRLQTLQHVREAGISVC	SID20	AWRETTIGRKNSNENQILEYVKE1RGGMGMEVCCCTLGMILEKQQAEEELKKAGLTAYNHNLDTSRSEYYPNIIISTSYSYDDRLQTLLEHVRREAGISIC	SID22	AWRETTIGRKNSNENQILEYVKE1RGGMGMEVCCCTLGMILEKQQAEEELKKAGLTAYNHNLDTSRSEYYPNIIISTSYSYDDRLQTLLEHVRREAGISIC	SID24	AWRETTIGRKNSNENQILEYVKE1RGGMGMEVCCCTLGMILEKQQAEEELKKAGLTAYNHNLDTSRSEYYPNIIISTSYSYDDRLQTLLEHVRREAGISIC	SID26	AWRDTIVGRKTNFQIILEYVKE1RGGMGMEVCCCTLGMILEKQQAEEELKKAGLTAYNHNLDTSRSEYYPNIIISTSYSYDDRLQTLLEHVRREAGISIC	SID28	AWRDTLGRKTNFQIILEYVVD1RDGMGMEVCCCTLGMILEKQQAEEELKKAGLTAYNHNLDTSRSEYYPNIIISTSYSYDDRLQTLLEHVRREAGINVC	SID32	AWRETTIGRKTNFQIILEYVVD1RDGMGMEVCCCTLGMILEKQQAEEELKKAGLTAYNHNLDTSRSEYYPNIIISTSYSYDDRLQTLLEHVRREAGINVC	1705463	AWRDTIGRKTNFQIILEYVVD1RDGMGMEVCCCTLGMILEKQQAEEELKKAGLTAYNHNLDTSRSEYYPNIIISTSYSYDDRLQTLLEHVRREAGISVC	SID30	AWRDMGRKTNLKVNKVTMVE1RGGMGMEVCVTLGMIDAEQAQELKEAGLTAYNHNVDTSRDFYPKVITRTTYDERLDTIKNVREAGINVC	2995363	AWRDLINGRNRTFKNILEI1KEVRSMMDMEVCVTLGMLINEQAQAKELKDAGLTAYNHNLDTSRSEYYSKILISTRRTYDERLNTLDNLRKAGLKVC	6321725	AWRDMKGKRSAMKRIQEMVTKVNNDMGLETCVTLGMVDQDQAKQLKDAGLTAYNHNLDTSRSEHYSKVITRTYDDRLQTLKNVQESGIKAC
SID18	SGGIIGLGGEAAEDRVGLLHTLATLPTPHESPVPINALTAVKGTPQD--QKP---VEIWEMIRMTASARIVMPKAMVRLSAGRVRFSMPE	SID20	SGGIIGLGGEAAEDRVGLLHTLATLPTPHESPVPINALVAVKGTPLED--QKP---VEIWEMIRMTATAR1TMPKAMVRLSAGRVRFSMPE	SID22	SGGIIGLGGEAAEDRVGLLHTLATLPTPHESPVPINALVAVKGTPLED--QKP---VEIWEMIRMTATAR1TMPKAMVRLSAGRVRFSMPE	SID24	SGGIIGLGGEAAEDRVGLLHTLATLPTPHESPVPINALVAVKGTPLED--QKP---VEIWEMIRMTATAR1TMPKAMVRLSAGRVRFSMPE	SID26	SGGIIGLGGEAAEDRVGLLHTLATLPTPHESPVPINALVAVKGTPLED--QKP---VEIWEMIRMTATAR1TMPKAMVRLSAGRVRFSMPE	SID28	SGGIIGLGGEAAEDRVGLLHTLATLPTPHESPVPINALVAVKGTPLED--QKP---VEIWEMIRMTATAR1TMPKAMVRLSAGRVRFSMSE	SID32	SGGIIGLGGEAAEDRVGLLHTLATLPTPHESPVPINALVAVKGTPLED--QKP---VEIWEMIRMTATAR1TMPKAMVRLSAGRVRFSMPE	1705463	SGGIIGLGGEAAEDRVGLLHTLATLPTPHESPVPINALIAVKGTPQD--QKP---VEIWEMIRMTASARIVMPKAMVRLSAGRVRFSMPE	SID30	TGGILGLGENKSDHIGLLETVALPSPHESPVPNMVAIKGTPLED--QKP---VEIWEMIRMTGATAR1VMPKAMVRLSAGRVRFSMSE	2995363	SGGILGLGEKHKDRVGLIHSLATMPTHESPVPFNLLVPIGTPV3DAVKER--LPIHPFLRSIATAR1CMPKTIIIRFAAAGRNTCSSE	6321725	TGGILGLGESEDDDHIGFYIYTLSNMSPHPESLP1NRLVAIKGTPMAEELADPKSKKLQDFEILRTIATARIVMPKAIIIRLAAGRYTMKTE
SID18	QALCFLAGANS1FAGEKLLTTANNDFDADQAMFKILGLIPKAP----NFGDEEATVASSTE--RCEQ--AASM	SID20	QALCFLAGANS1FAGEKLLTTANNDFDADQAMFKILGLIPKAP----SFGEAAAAPTESERSEQ--AASM	SID22	QALCFLAGANS1FAGEKLLTTANNDFDADQAMFKILGLIPKAP----SFGEAAAAPAESERSEQ--AASM	SID24	QALCFLAGANS1FAGEKLLTTANNDFDADQAMFKILGLIPKAP----SFGEAAAAPATESERSEQ--AASM	SID26	QALCFLAGANS1FTGEKLLTTPNNDFDADQMMFKILGLTPKAP----NFDQTS--TSFRAERCEQEATAS-	SID28	QALCFLAGANS1FTGEKLLTTPNNDFDADQMFKVLLGLPKAP----SLHEGE--TSVIEDY--KEAASSS	SID32	QALCFLAGANS1FAGEKLLTTANNDFDADQMFKILGLIPKAP----NFGDEEVMAAPTE--RCEQ--AALM	1705463	QALCFLAGANS1FTGEKLLTTPNNDFDADQMFKILGLIPKAP----SFSEDD--S--ESENCEKVASASH	SID30	QVLCFMAGANAVFTGETMLTTPAV7GNGVDSVVFNRFWGLRPMESEVEALKNDKPATNTNEIPVEASKAEMPGTV	2995363	QALAFMAGANAVFTGEKMLTTTPAVSNSDSDSQLFYNWGLEMQSFETYGT----STEGEDGTFPLPKERLAPSPL	6321725	QFVCFMAGANS1FTGKKM1TTMCNGWDEDKAMLKWLQPMEEAFKYD-----RS

FIGURE 2: Clone cdt2c.pk002.c17 Contains a 99 Nucleotide Deletion

SID19 CGACTGGAGCGCCGAGATCAGGCCGTCTACGACTCACCGCTCCTCGACCTCCTCTT
SID21 CGACTGGAGCGCCGAGATCAGGCCGTCTACGACTCACCGCTCCTCGACCTCCTCTT

SID19 TCACGGGGCTCAG--
SID21 TCACGGGGCTCAGTCCACAGAAATGTCCATAAATTCAAGAGAAGTGCAGCAATGCACACT

SID19 -----
SID21 TCTTTCAATCAAGACTGGTGGATGCAGTGAAAGATTGTCTTACTGTCCCTCAGTCATCAAG

SID19 ATACAACACTGGATTGAAGGCCAAAAATTGATGAACAAATATGCTGTCTGGAGGCAGC
SID21 ATACAACACTGGATTGAAGGCCAAAAATTGATGAACAAAGATGCTGTCTGGAGGCAGC